Nessendorf
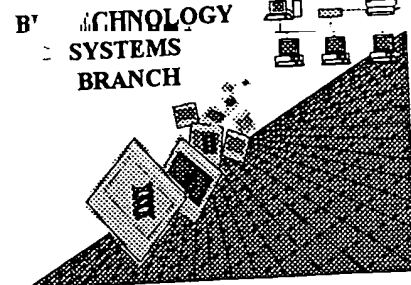
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: ___09/229,751___

Art Unit / Team No. : ___1618___

Date Processed by STIC: ___4/27/99___

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1. ☑ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2. ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3. ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4. ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5. ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6. ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7. ____ Wrong Designation
Sequence(s) ____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
_18,32-38,46-50,57-59,71-79,88-98,109_

8. ☑ Skipped Sequences (OLD RULES)
Sequence(s) __/__ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9. ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10. ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11. ____ Use of <213>Organism (NEW RULES)
Sequence(s) ____ are missing this mandatory field or its response.

12. ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> t <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13. ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/229,751*

INPUT SET: S31624.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: US PCT/US99/00771
66	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
87	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
108	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
129	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
150	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
171	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
192	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
213	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
234	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
255	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
276	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
297	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
318	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
399	Sequence 18 missing	(2) INFORMATION FOR SEQ ID NO:19:
672	Sequence 32 thru 38 missing	(2) INFORMATION FOR SEQ ID NO:39:
819	Sequence 46 thru 50 missing	(2) INFORMATION FOR SEQ ID NO:51:
946	Sequence 57 thru 59 missing	(2) INFORMATION FOR SEQ ID NO:60:
949	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
970	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
983	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
991	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1012	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1033	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1054	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1075	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1096	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1117	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1138	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1159	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1177	Sequence 71 thru 79 missing	(2) INFORMATION FOR SEQ ID NO:80:
1345	Sequence 88 thru 98 missing	(2) INFORMATION FOR SEQ ID NO:99:
1390	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1411	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1432	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1453	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1474	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1495	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1516	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1537	Entered (21) and Calc. Seq. Length (0) differ	(A) LENGTH: 21 base pairs
1555	Sequence 109 missing	(2) INFORMATION FOR SEQ ID NO:110:

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
 1                        SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: Turnbough Jr., Charles L
 6
 7        (ii) TITLE OF INVENTION: Peptide Ligands That Bind to Surfaces
 8   of
 9            Bacterial Spores
10
11    (iii) NUMBER OF SEQUENCES: 80
12
13   (iv) CORRESPONDENCE ADDRESS:
14            (A) ADDRESSEE: Hendricks and Associates
15            (B) STREET: P.O. Box 2509
16            (C) CITY: Fairfax
17            (D) STATE: VA
18            (E) COUNTRY: USA
19            (F) ZIP: 22031
20
21    (v) COMPUTER READABLE FORM:
22            (A) MEDIUM TYPE: Floppy disk
23            (B) COMPUTER: IBM PC compatible
24            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27    (vi) CURRENT APPLICATION DATA:
28            (A) APPLICATION NUMBER: US PCT/US99/00771
29            (B) FILING DATE: 14-JAN-1999
30            (C) CLASSIFICATION:
31
32   (viii) ATTORNEY/AGENT INFORMATION:
33            (A) NAME: Hendricks, Glenna M
34            (B) REGISTRATION NUMBER: 32,535
35            (C) REFERENCE/DOCKET NUMBER: turnbough
36
37   (ix) TELECOMMUNICATION INFORMATION:
38            (A) TELEPHONE: (703) 591-4470
39            (B) TELEFAX: (703) 591-4428
40
41
```

Handwritten annotations: "80///7 (see item 8 on Exam Summary Sheet)"; "These go under"; "(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE:"

ERRORED SEQUENCES FOLLOW:

```
63    (2) INFORMATION FOR SEQ ID NO:2:
64
65         (i) SEQUENCE CHARACTERISTICS:
66             (A) LENGTH: 21 base pairs
67             (B) TYPE: nucleic acid
68             (C) STRANDEDNESS: single
69             (D) TOPOLOGY: linear
70
71        (ii) MOLECULE TYPE: DNA (genomic)
72
73       (iii) HYPOTHETICAL: NO
74
75        (iv) ANTI-SENSE: NO
76
77
78
79        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
80
81    AATCATTTTT TGATTAAGCC G
82         21
83
```

global
for met eva
see item 1 on
Eva Summary Sheet
→ 21

```
84    (2) INFORMATION FOR SEQ ID NO:3:
85
86         (i) SEQUENCE CHARACTERISTICS:
87             (A) LENGTH: 21 base pairs
88             (B) TYPE: nucleic acid
89             (C) STRANDEDNESS: single
90             (D) TOPOLOGY: linear
91
92        (ii) MOLECULE TYPE: DNA (genomic)
93
94       (iii) HYPOTHETICAL: NO
95
96        (iv) ANTI-SENSE: NO
97
98
99
100       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
101
102   AATCATTTTT TGAGGTCTCC G
103        21
104
```

same
eva

```
105   (2) INFORMATION FOR SEQ ID NO:4:
106
107        (i) SEQUENCE CHARACTERISTICS:
108            (A) LENGTH: 21 base pairs
109            (B) TYPE: nucleic acid
110            (C) STRANDEDNESS: single
111            (D) TOPOLOGY: linear
112
113       (ii) MOLECULE TYPE: DNA (genomic)
```

PAGE: 3   **RAW SEQUENCE LISTING**
PATENT APPLICATION *US/09/229,751*   DATE: 04/27/1999
TIME: 10:35:29

INPUT SET: S31624.raw

```
114
115        (iii) HYPOTHETICAL: NO
116
117        (iv) ANTI-SENSE: NO
118
119
120
121        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
122
123   AATCATTTTC TGCCTCGTTG G
124        21
125
```

```
126   (2) INFORMATION FOR SEQ ID NO:5:
127
128        (i) SEQUENCE CHARACTERISTICS:
129             (A) LENGTH: 21 base pairs
130             (B) TYPE: nucleic acid
131             (C) STRANDEDNESS: single
132             (D) TOPOLOGY: linear
133
134        (ii) MOLECULE TYPE: DNA (genomic)
135
136        (iii) HYPOTHETICAL: NO
137
138        (iv) ANTI-SENSE: NO
139
140
141
142        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
143
144   AATCATTTTC TTCCTAAGGT G
145        21
146
```

```
147   (2) INFORMATION FOR SEQ ID NO:6:
148
149        (i) SEQUENCE CHARACTERISTICS:
150             (A) LENGTH: 21 base pairs
151             (B) TYPE: nucleic acid
152             (C) STRANDEDNESS: single
153             (D) TOPOLOGY: linear
154
155        (ii) MOLECULE TYPE: DNA (genomic)
156
157        (iii) HYPOTHETICAL: NO
158
159        (iv) ANTI-SENSE: NO
160
161
162
163        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
164
```

```
165    AATCATTTTC TGTTGCCGCC G
166        21
167

168    (2) INFORMATION FOR SEQ ID NO:7:
169
170        (i) SEQUENCE CHARACTERISTICS:
171            (A) LENGTH: 21 base pairs
172            (B) TYPE: nucleic acid
173            (C) STRANDEDNESS: single
174            (D) TOPOLOGY: linear
175
176        (ii) MOLECULE TYPE: DNA (genomic)
177
178        (iii) HYPOTHETICAL: NO
179
180        (iv) ANTI-SENSE: NO
181
182.
183
184        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
185
186    AATCATTTTT TGCCTCCTCG G
187        21
188

189    (2) INFORMATION FOR SEQ ID NO:8:
190
191        (i) SEQUENCE CHARACTERISTICS:
192            (A) LENGTH: 21 base pairs
193            (B) TYPE: nucleic acid
194            (C) STRANDEDNESS: single
195            (D) TOPOLOGY: linear
196
197        (ii) MOLECULE TYPE: DNA (genomic)
198
199        (iii) HYPOTHETICAL: NO
200
201        (iv) ANTI-SENSE: NO
202
203
204
205        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
206
207    AATCATTTTC TGCCTACTGG G
208        21
209

210    (2) INFORMATION FOR SEQ ID NO:9:
211
212        (i) SEQUENCE CHARACTERISTICS:
213            (A) LENGTH: 21 base pairs
214            (B) TYPE: nucleic acid
```

```
215          (C) STRANDEDNESS: single
216          (D) TOPOLOGY: linear
217
218     (ii) MOLECULE TYPE: DNA (genomic)
219
220    (iii) HYPOTHETICAL: NO
221
222     (iv) ANTI-SENSE: NO
223
224
225
226     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
227
228  AATCATTTTC TGATGCCGAA G
229        21
230
```

```
231  (2) INFORMATION FOR SEQ ID NO:10:
232
233      (i) SEQUENCE CHARACTERISTICS:
234          (A) LENGTH: 21 base pairs
235          (B) TYPE: nucleic acid
236          (C) STRANDEDNESS: single
237          (D) TOPOLOGY: linear
238
239     (ii) MOLECULE TYPE: DNA (genomic)
240
241    (iii) HYPOTHETICAL: NO
242
243     (iv) ANTI-SENSE: NO
244
245
246
247     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
248
249  AATCATTTTC TTAAGGGGAC G
250        21
251
```

```
252  (2) INFORMATION FOR SEQ ID NO:11:
253
254      (i) SEQUENCE CHARACTERISTICS:
255          (A) LENGTH: 21 base pairs
256          (B) TYPE: nucleic acid
257          (C) STRANDEDNESS: single
258          (D) TOPOLOGY: linear
259
260     (ii) MOLECULE TYPE: DNA (genomic)
261
262    (iii) HYPOTHETICAL: NO
263
264     (iv) ANTI-SENSE: NO
265
```

```
266
267
268        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
269
270    ATTCATTTTT TGCCGCAGAA T
271        21
272
```

```
273    (2) INFORMATION FOR SEQ ID NO:12:
274
275        (i) SEQUENCE CHARACTERISTICS:
276            (A) LENGTH: 21 base pairs
277            (B) TYPE: nucleic acid
278            (C) STRANDEDNESS: single
279            (D) TOPOLOGY: linear
280
281        (ii) MOLECULE TYPE: DNA (genomic)
282
283       (iii) HYPOTHETICAL: NO
284
285        (iv) ANTI-SENSE: NO
286
287
288
289        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
290
291    ATTCATTTTC TTCTTTGGCG T
292        21
293
```

```
294    (2) INFORMATION FOR SEQ ID NO:13:
295
296        (i) SEQUENCE CHARACTERISTICS:
297            (A) LENGTH: 21 base pairs
298            (B) TYPE: nucleic acid
299            (C) STRANDEDNESS: single
300            (D) TOPOLOGY: linear
301
302        (ii) MOLECULE TYPE: DNA (genomic)
303
304       (iii) HYPOTHETICAL: NO
305
306        (iv) ANTI-SENSE: NO
307
308
309
310        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
311
312    AATCATTTTC TGATTAGGAA G
313        21
314
```

```
315    (2) INFORMATION FOR SEQ ID NO:14:
```

```
316
317        (i)  SEQUENCE CHARACTERISTICS:
318             (A)  LENGTH: 21 base pairs
319             (B)  TYPE: nucleic acid
320             (C)  STRANDEDNESS: single
321             (D)  TOPOLOGY: linear
322
323       (ii)  MOLECULE TYPE: DNA (genomic)
324
325      (iii)  HYPOTHETICAL: NO
326
327       (iv)  ANTI-SENSE: NO
328
329
330
331       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:14:
332
333   AATCATTTTC TGCCGACTGC T
334        21
335
```

same error (handwritten)

Seq 18 missing (see back pages) (handwritten)

```
399   (2) INFORMATION FOR SEQ ID NO:19:
400
401        (i)  SEQUENCE CHARACTERISTICS:
402             (A)  LENGTH: 7 amino acids
403             (B)  TYPE: amino acid
404             (C)  STRANDEDNESS: single
405             (D)  TOPOLOGY: linear
406
407       (ii)  MOLECULE TYPE: peptide
408
409      (iii)  HYPOTHETICAL: NO
410
411       (iv)  ANTI-SENSE: NO
412
413
414
415       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:19:
416
417       Asn His Phe Leu Ile Lys Pro
418        1                   5
419
```

OK (handwritten)

Seqs 32 through 38 missing (back pages) (handwritten)

```
672   (2) INFORMATION FOR SEQ ID NO:39:
673
674        (i)  SEQUENCE CHARACTERISTICS:
675             (A)  LENGTH: 5 amino acids
676             (B)  TYPE: amino acid
677             (C)  STRANDEDNESS: single
678             (D)  TOPOLOGY: linear
679
680       (ii)  MOLECULE TYPE: peptide
681
```

INPUT SET: S31624.raw

```
682        (iii) HYPOTHETICAL: NO
683
684        (iv) ANTI-SENSE: NO
685
686
687
688        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
689
690          Asn His Phe Leu Pro
691          1               5
692
```

Seq 46 through 50 missing

(back pages)

```
-->   819   (2) INFORMATION FOR SEQ ID NO:51:
      820
      821        (i) SEQUENCE CHARACTERISTICS:
      822             (A) LENGTH: 7 amino acids
      823             (B) TYPE: amino acid
      824             (C) STRANDEDNESS: single
      825             (D) TOPOLOGY: linear
      826
      827        (ii) MOLECULE TYPE: peptide
      828
      829        (iii) HYPOTHETICAL: NO
      830
      831        (iv) ANTI-SENSE: NO
      832
      833
      834
      835        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
      836
      837          Lys Pro Arg Gln Pro Gly Leu
      838          1               5
      839
```

OK

Seq 57 through 59 missing

(back pages)

```
-->   946   (2) INFORMATION FOR SEQ ID NO:60:
      947
      948        (i) SEQUENCE CHARACTERISTICS:
-->   949             (A) LENGTH: 21 base pairs
      950             (B) TYPE: nucleic acid
      951             (C) STRANDEDNESS: single
      952             (D) TOPOLOGY: linear
      953
      954        (ii) MOLECULE TYPE: DNA (genomic)
      955
      956        (iii) HYPOTHETICAL: NO
      957
      958        (iv) ANTI-SENSE: NO
      959
      960
      961
      962        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
      963
      964   AATAGTGTTA CTCTTGAGCC G
```

same format error as displayed in previous sequences

```
965        21
966
```

```
967    (2) INFORMATION FOR SEQ ID NO:61:
968
969        (i) SEQUENCE CHARACTERISTICS:
-->  970             (A) LENGTH: 21 base pairs
971                 (B) TYPE: nucleic acid
972                 (C) STRANDEDNESS: single
973                 (D) TOPOLOGY: linear
974
975        (ii) MOLECULE TYPE: DNA (genomic)
976
977        (iii) HYPOTHETICAL: NO
978
979        (iv) ANTI-SENSE: NO
980
981
982
-->  983        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
984
985    AAGCCGAGGC AGCCGGGTTT G
986        21
987
```

```
988    (2) INFORMATION FOR SEQ ID NO:62:
989
990        (i) SEQUENCE CHARACTERISTICS:
-->  991             (A) LENGTH: 21 base pairs
992                 (B) TYPE: nucleic acid
993                 (C) STRANDEDNESS: single
994                 (D) TOPOLOGY: linear
995
996        (ii) MOLECULE TYPE: DNA (genomic)
997
998        (iii) HYPOTHETICAL: NO
999
1000        (iv) ANTI-SENSE: NO
1001
1002
1003
1004        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
1005
1006    TCTACTCCGG CGTGGCTGTC G
1007        21
1008
```

```
1009    (2) INFORMATION FOR SEQ ID NO:63:
1010
1011        (i) SEQUENCE CHARACTERISTICS:
-->  1012             (A) LENGTH: 21 base pairs
1013                 (B) TYPE: nucleic acid
1014                 (C) STRANDEDNESS: single
```

```
1015                    (D) TOPOLOGY: linear
1016
1017          (ii) MOLECULE TYPE: DNA (genomic)
1018
1019         (iii) HYPOTHETICAL: NO
1020
1021          (iv) ANTI-SENSE: NO
1022
1023
1024
1025          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
1026
1027   ACTAGTCAGA ATGTGCGGAC G
1028        21
1029
```

```
1030   (2) INFORMATION FOR SEQ ID NO:64:
1031
1032          (i) SEQUENCE CHARACTERISTICS:
1033              (A) LENGTH: 21 base pairs
1034              (B) TYPE: nucleic acid
1035              (C) STRANDEDNESS: single
1036              (D) TOPOLOGY: linear
1037
1038          (ii) MOLECULE TYPE: DNA (genomic)
1039
1040         (iii) HYPOTHETICAL: NO
1041
1042          (iv) ANTI-SENSE: NO
1043
1044
1045
1046          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
1047
1048   ACTTATCCTA TTCCGATTCG T
1049        21
1050
```

```
1051   (2) INFORMATION FOR SEQ ID NO:65:
1052
1053          (i) SEQUENCE CHARACTERISTICS:
1054              (A) LENGTH: 21 base pairs
1055              (B) TYPE: nucleic acid
1056              (C) STRANDEDNESS: single
1057              (D) TOPOLOGY: linear
1058
1059          (ii) MOLECULE TYPE: DNA (genomic)
1060
1061         (iii) HYPOTHETICAL: NO
1062
1063          (iv) ANTI-SENSE: NO
1064
1065
```

```
1066
1067        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
1068
1069   ACTTATCCTA TTCCGTTTCG T
1070        21
1071
```

```
1072   (2) INFORMATION FOR SEQ ID NO:66:
1073
1074        (i) SEQUENCE CHARACTERISTICS:
1075            (A) LENGTH: 21 base pairs
1076            (B) TYPE: nucleic acid
1077            (C) STRANDEDNESS: single
1078            (D) TOPOLOGY: linear
1079
1080       (ii) MOLECULE TYPE: DNA (genomic)
1081
1082      (iii) HYPOTHETICAL: NO
1083
1084       (iv) ANTI-SENSE: NO
1085
1086
1087
1088        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1089
1090   TCTTATCCTC ATGGTCAGAT T
1091        21
1092
```

```
1093   (2) INFORMATION FOR SEQ ID NO:67:
1094
1095        (i) SEQUENCE CHARACTERISTICS:
1096            (A) LENGTH: 21 base pairs
1097            (B) TYPE: nucleic acid
1098            (C) STRANDEDNESS: single
1099            (D) TOPOLOGY: linear
1100
1101       (ii) MOLECULE TYPE: DNA (genomic)
1102
1103      (iii) HYPOTHETICAL: NO
1104
1105       (iv) ANTI-SENSE: NO
1106
1107
1108
1109        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
1110
1111   TTTACTGGGA CTCTTAATCC T
1112        21
1113
```

```
1114   (2) INFORMATION FOR SEQ ID NO:68:
1115
```

INPUT SET: S31624.raw

```
1116          (i) SEQUENCE CHARACTERISTICS:
1117              (A) LENGTH: 21 bas  pairs
1118              (B) TYPE: nucleic acid
1119              (C) STRANDEDNESS: single
1120              (D) TOPOLOGY: linear
1121
1122      (ii) MOLECULE TYPE: DNA (genomic)
1123
1124      (iii) HYPOTHETICAL: NO
1125
1126      (iv) ANTI-SENSE: NO
1127
1128
1129
1130      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
1131
1132  ACTTATCCGG TGCCGCATCG G
1133          21
1134
```

```
1135  (2) INFORMATION FOR SEQ ID NO:69:
1136
1137          (i) SEQUENCE CHARACTERISTICS:
1138              (A) LENGTH: 21 base pairs
1139              (B) TYPE: nucleic acid
1140              (C) STRANDEDNESS: single
1141              (D) TOPOLOGY: linear
1142
1143      (ii) MOLECULE TYPE: DNA (genomic)
1144
1145      (iii) HYPOTHETICAL: NO
1146
1147      (iv) ANTI-SENSE: NO
1148
1149
.1150
1151      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1152
1153  CGGACTCCTT CGCTTCCTAG T
1154          21
1155
```

```
1156  (2) INFORMATION FOR SEQ ID NO:70:
1157
1158          (i) SEQUENCE CHARACTERISTICS:
1159              (A) LENGTH: 21 base pairs
1160              (B) TYPE: nucleic acid
1161              (C) STRANDEDNESS: single
1162              (D) TOPOLOGY: linear
1163
1164      (ii) MOLECULE TYPE: DNA (genomic)
1165
1166      (iii) HYPOTHETICAL: NO
```

```
1167
1168        (iv) ANTI-SENSE: NO
1169
1170
1171
1172        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
1173
1174   TTTAGTGTTC CTCGTATGCC G
1175        21
1176
```

--> `1177   (2) INFORMATION FOR SEQ ID NO:80:`

```
1178
1179        (i) SEQUENCE CHARACTERISTICS:
1180            (A) LENGTH: 12 amino acids
1181            (B) TYPE: amino acid
1182            (C) STRANDEDNESS: single
1183            (D) TOPOLOGY: linear
1184
1185       (ii) MOLECULE TYPE: peptide
1186
1187      (iii) HYPOTHETICAL: NO
1188
1189       (iv) ANTI-SENSE: NO
1190
1191
1192
1193       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
1194
1195   Asn His Phe Leu Lys Ser Gln Pro Gly Val Val Thr
1196    1              5              10
1197
```

--> `1345   (2) INFORMATION FOR SEQ ID NO:99:`

```
1346
1347        (i) SEQUENCE CHARACTERISTICS:
1348            (A) LENGTH: 11 amino acids
1349            (B) TYPE: amino acid
1350            (C) STRANDEDNESS: single
1351            (D) TOPOLOGY: linear
1352
1353       (ii) MOLECULE TYPE: peptide
1354
1355      (iii) HYPOTHETICAL: NO
1356
1357       (iv) ANTI-SENSE: NO
1358
1359
1360
1361       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
1362
1363   Asn His Phe Leu Pro Lys Val Gly Gly Gly Cys
1364    1              5              10
```

INPUT SET: S31624.raw

```
      1365
```

```
      1387   (2) INFORMATION FOR SEQ ID NO:101:
      1388
      1389        (i) SEQUENCE CHARACTERISTICS:
-->   1390            (A) LENGTH: 21 base pairs
      1391            (B) TYPE: nucleic acid
      1392            (C) STRANDEDNESS: single
      1393            (D) TOPOLOGY: linear
      1394
      1395       (ii) MOLECULE TYPE: DNA (genomic)
      1396
      1397      (iii) HYPOTHETICAL: NO
      1398
      1399       (iv) ANTI-SENSE: NO
      1400
      1401
      1402
      1403        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
      1404
      1405   ACGCATCGTT TGCCTTCTCG G
      1406        21
      1407
```

format error

```
      1408   (2) INFORMATION FOR SEQ ID NO:102:
      1409
      1410        (i) SEQUENCE CHARACTERISTICS:
-->   1411            (A) LENGTH: 21 base pairs
      1412            (B) TYPE: nucleic acid
      1413            (C) STRANDEDNESS: single
      1414            (D) TOPOLOGY: linear
      1415
      1416       (ii) MOLECULE TYPE: DNA (genomic)
      1417
      1418      (iii) HYPOTHETICAL: NO
      1419
      1420       (iv) ANTI-SENSE: NO
      1421
      1422
      1423
      1424        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
      1425
      1426   GTTACTAGTA GGGGGAATGT T
      1427        21
      1428
```

```
      1429   (2) INFORMATION FOR SEQ ID NO:103:
      1430
      1431        (i) SEQUENCE CHARACTERISTICS:
-->   1432            (A) LENGTH: 21 base pairs
      1433            (B) TYPE: nucleic acid
      1434            (C) STRANDEDNESS: single
      1435            (D) TOPOLOGY: linear
```

```
1436
1437        (ii) MOLECULE TYPE: DNA (genomic)
1438
1439     (iii) HYPOTHETICAL: NO
1440
1441      (iv) ANTI-SENSE: NO
1442
1443
1444
1445       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
1446
1447   AAGCTGTGGG TGATTCCTCA G
1448         21
1449
```

```
1450   (2) INFORMATION FOR SEQ ID NO:104:
1451
1452        (i) SEQUENCE CHARACTERISTICS:
1453           (A) LENGTH: 21 base pairs
1454           (B) TYPE: nucleic acid
1455           (C) STRANDEDNESS: single
1456           (D) TOPOLOGY: linear
1457
1458       (ii) MOLECULE TYPE: DNA (genomic)
1459
1460     (iii) HYPOTHETICAL: NO
1461
1462      (iv) ANTI-SENSE: NO
1463
1464
1465
1466       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
1467
1468   TATTCGCCTC CTCATAGGCA T
1469         21
1470
```

```
1471   (2) INFORMATION FOR SEQ ID NO:105:
1472
1473        (i) SEQUENCE CHARACTERISTICS:
1474           (A) LENGTH: 21 base pairs
1475           (B) TYPE: nucleic acid
1476           (C) STRANDEDNESS: single
1477           (D) TOPOLOGY: linear
1478
1479       (ii) MOLECULE TYPE: DNA (genomic)
1480
1481     (iii) HYPOTHETICAL: NO
1482
1483      (iv) ANTI-SENSE: NO
1484
1485
1486
```

INPUT SET: S31624.raw

```
1487        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
1488
1489     TCGTATCCTC CGTATTTTGA T
1490         21
1491
```

```
1492     (2) INFORMATION FOR SEQ ID NO:106:
1493
1494          (i) SEQUENCE CHARACTERISTICS:
-->  1495             (A) LENGTH: 21 base pairs
1496             (B) TYPE: nucleic acid
1497             (C) STRANDEDNESS: single
1498             (D) TOPOLOGY: linear
1499
1500         (ii) MOLECULE TYPE: DNA (genomic)
1501
1502        (iii) HYPOTHETICAL: NO
1503
1504         (iv) ANTI-SENSE: NO
1505
1506
1507
1508          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:
1509
1510     CTTTTGTCGC CTCTGCATCG T
1511         21
1512
```

```
1513     (2) INFORMATION FOR SEQ ID NO:107:
1514
1515          (i) SEQUENCE CHARACTERISTICS:
-->  1516             (A) LENGTH: 21 base pairs
1517             (B) TYPE: nucleic acid
1518             (C) STRANDEDNESS: single
1519             (D) TOPOLOGY: linear
1520
1521         (ii) MOLECULE TYPE: DNA (genomic)
1522
1523        (iii) HYPOTHETICAL: NO
1524
1525         (iv) ANTI-SENSE: NO
1526
1527
1528
1529          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
1530
1531     TTTGATTCTC CGCTTCGTCG G
1532         21
1533
```

```
1534     (2) INFORMATION FOR SEQ ID NO:108:
1535
1536          (i) SEQUENCE CHARACTERISTICS:
```

INPUT SET: S31624.raw

```
-->   1537              (A) LENGTH: 21 base pairs
      1538              (B) TYPE: nucleic acid
      1539              (C) STRANDEDNESS: single
      1540              (D) TOPOLOGY: linear
      1541
      1542        (ii) MOLECULE TYPE: DNA (genomic)
      1543
      1544        (iii) HYPOTHETICAL: NO
      1545
      1546        (iv) ANTI-SENSE: NO
      1547
      1548
      1549
      1550        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:
      1551
      1552   TGGTCGCCGC TGCATAAGCA T
      1553        21
      1554
```

same

Seq 109 missing
(back page)

```
-->   1555   (2) INFORMATION FOR SEQ ID NO:110:
      1556
      1557        (i) SEQUENCE CHARACTERISTICS:
      1558              (A) LENGTH: 7 amino acids
      1559              (B) TYPE: amino acid
      1560              (C) STRANDEDNESS: single
      1561              (D) TOPOLOGY: linear
      1562
      1563        (ii) MOLECULE TYPE: peptide
      1564
      1565        (iii) HYPOTHETICAL: NO
      1566
      1567        (iv) ANTI-SENSE: NO
      1568
      1569
      1570
      1571        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
      1572
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Phe Asn Lys His Val Pro Gly Gly Gly Cys
1   5   10

Seq 18 missing

(see item 8 on Exam

Summary Sheet)

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

 (iii) HYPOTHETICAL: NO

  (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn His Phe Leu Pro Thr Ala
1   5

(2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asn Ser Val Thr Leu Glu Pro
1   5

(2) INFORMATION FOR SEQ ID NO:51:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 7 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe Ser Val Pro Arg Met Pro
1   5

Seq 57 through 59 missing

(2) INFORMATION FOR SEQ ID NO:60:

    (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TTTAGTGTTC CTCGTATGCC G
    21

(2) INFORMATION FOR SEQ ID NO:80:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids

Seqs 71 through 79 missing

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Asn His Phe Leu Met Pro Asn Pro Leu Leu Ala Met
1   5   10

Sep 88 through 98 missing

(2) INFORMATION FOR SEQ ID NO:99:

    (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGGTCGCCGC TGCATAAGCA T   *former*   → *Seq 109 missing*
    21

(2) INFORMATION FOR SEQ ID NO:110: